



## SEQUENCE LISTING

<110> Caput, Daniel  
Ferrara, Pascual  
Laurent, Patrick  
Vita, Natalio

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<141> 1998-09-14

<150> PCT/FR96/01756

<151> 1996-11-07

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<170> PatentIn Ver. 2.0

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<212> DNA

<213> Homo sapiens

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<212> PRT 3

<213> Homo sapiens

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Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
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Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
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Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
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Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
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Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
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Val	Leu	Ile	Glu	Asn	Leu	Lys	Lys	Ala	Ser	Gln					
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&lt;210&gt; 5

&lt;211&gt; 420

&lt;212&gt; PRT 3

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

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          20           25           30
Pro Val Asn Phe Thr Ile Lys Val Thr Gly Leu Ala Gln Val Leu Leu
          35           40           45
Gln Trp Lys Pro Asn Pro Asp Gln Glu Gln Arg Asn Val Asn Leu Glu
          50           55           60
Tyr Gln Val Lys Ile Asn Ala Pro Lys Glu Asp Asp Tyr Glu Thr Arg
 65           70           75           80
Ile Thr Glu Ser Lys Cys Val Thr Ile Leu His Lys Gly Phe Ser Ala
          85           90           95
Ser Val Arg Thr Ile Leu Gln Asn Asp His Ser Leu Leu Ala Ser Ser
          100          105          110
Trp Ala Ser Ala Glu Leu His Ala Pro Pro Gly Ser Pro Gly Thr Ser
          115          120          125
Ile Val Asn Leu Thr Cys Thr Thr Asn Thr Thr Glu Asp Asn Tyr Ser
 130          135          140
Arg Leu Arg Ser Tyr Gln Val Ser Leu His Cys Thr Trp Leu Val Gly
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Thr Asp Ala Pro Glu Asp Thr Gln Tyr Phe Leu Tyr Tyr Arg Tyr Gly
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Ser Trp Thr Glu Glu Cys Gln Glu Tyr Ser Lys Asp Thr Leu Gly Arg
          180          185          190
Asn Ile Ala Cys Trp Phe Pro Arg Thr Phe Ile Leu Ser Lys Gly Arg
          195          200          205
Asp Trp Leu Ser Val Leu Val Asn Gly Ser Ser Lys His Ser Ala Ile
 210          215          220
Arg Pro Phe Asp Gln Leu Phe Ala Leu His Ala Ile Asp Gln Ile Asn
 225          230          235          240
Pro Pro Leu Asn Val Thr Ala Glu Ile Glu Gly Thr Arg Leu Ser Ile
          245          250          255
Gln Trp Glu Lys Pro Val Ser Ala Phe Pro Ile His Cys Phe Asp Tyr
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Glu Val Lys Ile His Asn Thr Arg Asn Gly Tyr Leu Gln Ile Glu Lys
 275          280          285
Leu Met Thr Asn Ala Phe Ile Ser Ile Ile Asp Asp Leu Ser Lys Tyr
 290          295          300
Asp Val Gln Val Arg Ala Ala Val Ser Ser Met Cys Arg Glu Ala Gly
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Leu Trp Ser Glu Trp Ser Gln Pro Ile Tyr Val Gly Asn Asp Glu His
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Lys Pro Leu Arg Glu Trp Phe Val Ile Val Ile Met Ala Thr Ile Cys
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Thr	Trp	Ser	Pro	Pro	Glu	Gly	Ala	Ser	Pro	Asn	Cys	Thr	Leu	Arg	Tyr	50	55	60	
Phe	Ser	His	Phe	Asp	Asp	Gln	Gln	Asp	Lys	Lys	Ile	Ala	Pro	Glu	Thr	65	70	75	80
His	Arg	Lys	Glu	Glu	Leu	Pro	Leu	Asp	Glu	Lys	Ile	Cys	Leu	Gln	Val	85	90	95	
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Trp	Tyr	Ser	Ser	Leu	Glu	Lys	Ser	Arg	Gln	Cys	Glu	Asn	Ile	Tyr	Arg	165	170	175	
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Pro	Asp	Pro	Pro	His	Ile	Lys	His	Leu	Leu	Leu	Lys	Asn	Gly	Ala	Leu	225	230	235	240
Leu	Val	Gln	Trp	Lys	Asn	Pro	Gln	Asn	Phe	Arg	Ser	Arg	Cys	Leu	Thr	245	250	255	
Tyr	Glu	Val	Glu	Val	Asn	Asn	Thr	Gln	Thr	Asp	Arg	His	Asn	Ile	Leu				

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 20 25 30

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Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
   35                               40   45
Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser Leu Asp His Phe Lys Glu
   50                               55   60
Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Gly Ser Glu Thr
   65                               70   75   80
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
   85                               90   95
Leu Asn Lys Gly Ile Glu Ala Lys Ile His Thr Leu Leu Pro Trp Gln
  100                               105  110
Cys Thr Asn Gly Ser Glu Val Gln Ser Ser Trp Ala Glu Thr Thr Tyr
  115                               120  125
Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr Lys Val Gln Asp Met Asp
  130                               135  140
Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu Cys Ser Trp Lys Pro Gly
  145                               150  155  160
Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn Leu Phe Tyr Trp Tyr Glu
  165                               170  175
Gly Leu Asp His Ala Leu Gln Cys Val Asp Tyr Ile Lys Ala Asp Gly
  180                               185  190
Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu Glu Ala Ser Asp Tyr Lys
  195                               200  205
Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Asn Lys Pro Ile Arg
  210                               215  220
Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn Ile Val Lys Pro Leu Pro
  225                               230  235  240
Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser Ser Cys Glu Ile Lys Leu
  245                               250  255
Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro Ala Arg Cys Phe Asp Tyr
  260                               265  270
Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr Leu Val Thr Ala Thr Val
  275                               280  285
Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr Asn Glu Thr Arg Gln Leu
  290                               295  300
Cys Phe Val Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly
  305                               310  315  320
Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys Trp Glu Gly Glu Asp Leu
  325                               330  335
Ser Lys Lys Thr Leu Leu Arg Phe Trp Leu Pro Phe Gly Phe Ile Leu
  340                               345  350
Ile Leu Val Ile Phe Val Thr Gly Leu Leu Leu Arg Lys Pro Asn Thr
  355                               360  365
Tyr Pro Lys Met Val Arg Cys Val Thr Leu
  370                               375

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<210> 13

<211> 5

<212> PRT 3

<213> Artificial sequence

<220>

<222> (1)...(5)

<223> motif characteristic of the family of chemokine receptors to which the polypeptides of SEQ ID NO. 2 and SEQ NO. 4 belong.

<223> Xaa can be any amino acid.

<400> 13

Trp Ser Xaa Trp Ser  
1 5

<210> 14

<211> 6

<212> DNA

<213> Artificial sequence

<220>

<223> polyadenylation signal

<400> 14

aataaaa 6

<210> 15

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 15

aaaaaaaaaa aaagggcccg 20